

1631

OIPE

#4

P.S

RAW SEQUENCE LISTING

DATE: 06/07/2000

PATENT APPLICATION: US/09/521,640

TIME: 11:22:31

Input Set : D:\BACENDTAB_FINAL_RETREATS.rpt

Output Set: N:\CRF3\06072000\I521640.raw

ENTERED

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1 <110> APPLICANT: Byrum, Joseph R.
2   Halling, Conrad H.
3   Kovalic, David K.
5 <120> TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
6   Plants
8 <130> FILE REFERENCE: 38-21(15750)D
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/521,640
C--> 10 <141> CURRENT FILING DATE: 2000-03-10
10 <160> NUMBER OF SEQ ID NOS: 304701
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 619
14 <212> TYPE: DNA
15 <213> ORGANISM: Glycine max
17 <223> OTHER INFORMATION: unsure at all n locations
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W--> 22 aatttgaccg ctggaacata cattggcttt ttagcntgaa tcgcctattg catgaacaac 120
W--> 24 attcaaaaaca actaaatngc cttgggctta gcgagactga ctgcgttanc ccatgcttat 180
26 tcaaaactata taggcatggt gtcttagcag gactgactct cttatccacc aacagaatac 240
W--> 28 cacaagcctc atagactccg acctaagcaa actaactcgc ttatcacggc atgtcngcta 300
W--> 30 tcaagttcat actaactcag aagatataac tagagatnta tactcttngc tagccgaagt 360
W--> 32 gcaggggctt aacgagttcg tcataaaaagc atagatttaa catanatgat gaacatgctt 420
W--> 34 agcgggacaa gaccgactta ctgatgtcat catataaccc anaatatcat ccanaataat 480
W--> 36 agactggcta ntgagcagct cgctagcaga catcaaagtt cagaaatatg nggctcaaga 540
38 cccacatcta gtactatatg ctatactata gtcaaacatg aatgacctca tatcctgaat 600
40 aatccctaca ctatagtag 619
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 465
45 <212> TYPE: DNA
46 <213> ORGANISM: Glycine max
48 <223> OTHER INFORMATION: unsure at all n locations
W--> 49 <400> SEQUENCE: 2
51 ggggagatgc gtgagttcac tcaatattag cccttcagac tcgctgtaag acctcggctc 60
53 agccgaatcc ctttatgagc gcttaagtca ctgccgcgct tacacgcgga ctgagaaacc 120
55 tgcgtacccg ctaatctctt cacacatccc ctatcgact ggcggtatct caatgaccac 180
57 catcgcttc caaccatgcc aactaatggc aatggccctg atcggatttc tcttaccatt 240
59 gtcggattta cccgctatgg cgcttcacac acagaggatg ccctagtatc accctaccac 300
61 caccocgtga ccaaccttgg cctttaaata aaacctatct ttgtcatttc ggaataaact 360
W--> 63 ttcctgtctt tcagcaaatg aagaaccctt gctcgtcct ttgggcgggc cttttgcacg 420
W--> 65 ctttttgagc ttgttatcaa aaaaaccctt cttgttcaaa acacn 465
68 <210> SEQ ID NO: 3
69 <211> LENGTH: 175
70 <212> TYPE: DNA
71 <213> ORGANISM: Glycine max
73 <400> SEQUENCE: 3
75 ggacttagta cgcgcttact gttacatata ctacctatgg caaatttggt ttacactgaa 60
77 ttacaacctt gtatgcacaa cgtatggtac tcctttttgt tgcagttagt gaccattggg 120

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79 gagtatgaac aggcgatgaaa acacttaaag tcactttgga ataacacgac aaggt      175
82 <210> SEQ ID NO: 4
83 <211> LENGTH: 247
84 <212> TYPE: DNA
85 <213> ORGANISM: Glycine max
87 <223> OTHER INFORMATION: unsure at all n locations
W--> 88 <400> SEQUENCE: 4
W--> 90 tctatacctg ttgcaagagn ttgtgggtcta cgttcttctg cagatcacca tacagatctc      60
92 tgtccttctt ttagcaatc tggagtcagt gagaaacctg aagcttatgc tgtaaacatt      120
W--> 94 tataatagac ctctcagca acanaactaa caacagcaga ataattatga cctttcaagc      180
W--> 96 aatagatgca atctaggttg gaggaatcat ccaaatctga gatggacaag tntccgcaa      240
98 caacaac      247
101 <210> SEQ ID NO: 5
102 <211> LENGTH: 337
103 <212> TYPE: DNA
104 <213> ORGANISM: Glycine max
106 <223> OTHER INFORMATION: unsure at all n locations
W--> 107 <400> SEQUENCE: 5
109 gagtctctc acgagtgga ggttgagcca tgttctcagt ataaaaatta gtagtggaa      60
W--> 111 gctcanaatc agaatttca aaatcaccct caagagaatg etcaccaatgc acataatgac      120
113 caggatgcac agtatgccta attaatctat gaaaggatct atctatttca agatcaaaag      180
115 gtgtgaaatc acctagaatg ccctagtca tgcactatat ccagcaata atgtgtttct      240
W--> 117 taacaagcac ctaaccagn ggtaaaaact caactatact caaacgatat caaaatgagc      300
W--> 119 cttaaatattg tgaggaacac cctanaatca tgaaaag      337
122 <210> SEQ ID NO: 6
123 <211> LENGTH: 211
124 <212> TYPE: DNA
125 <213> ORGANISM: Glycine max
127 <223> OTHER INFORMATION: unsure at all n locations
W--> 128 <400> SEQUENCE: 6
W--> 130 gagatgatgc gctccatgag tatgtggatc anatggagaa tagagatcat aatgaagaag      60
132 aaaggaggag aagagggaat gatgggtgttc ctagacaaaa ccgaattgat ggtattaaac      120
134 tcaacattcc tccatttaaa ggaagagaatg atccggaggc ctacgtggag tgggagatga      180
136 aatagagca tgttttctca tgcaacaact a      211
139 <210> SEQ ID NO: 7
140 <211> LENGTH: 482
141 <212> TYPE: DNA
142 <213> ORGANISM: Glycine max
144 <223> OTHER INFORMATION: unsure at all n locations
W--> 145 <400> SEQUENCE: 7
W--> 147 agcctgtgtc ctgaanattt gaanntcatt cacctgaggt ggcnacctct gaacttctac      60
149 agaatgagct ctgatccact ggtatacaag ggcctcagat atcttaagaa cggggggttg      120
151 attaagatat taccactat ttccccagt aaaaatctat ttcactttct atttcaggta      180
153 ccaaatccct taaccatgga ctcttaata atgattccaa ttgaaccatt ttgatgttaa      240
W--> 155 tataaaacca ttattaatta aagaagttca cggaagagaa agtgcanacc tggatttata      300
157 ctgggtcggg acacctgtgt ctacgtccgt cccagaaccg ctgaagtcatt attgaaatct      360
159 tcagttgaca cagcatctct ggtaatttca caaacctgtt atcttgataa aaagaatact      420
161 ttgaaatatt ctgcccagt ctagatgagg tgcagattaa gaaagttgtt aaaacctggt      480
163 aa      482

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Input Set : D:\BACENDTAB_FINAL_RETREATS.rpt
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166 <210> SEQ ID NO: 8
167 <211> LENGTH: 574
168 <212> TYPE: DNA
169 <213> ORGANISM: Glycine max
171 <223> OTHER INFORMATION: unsure at all n locations
W--> 172 <400> SEQUENCE: 8
W--> 174 ntatcacttg aggacctatg atactaagct ctataaagtt acttgctgaa ccaatcaa 60
W--> 176 aagttttcaa ctagtataaa atgttagaaa tttatgtgaa atttntacca aagatagtca 120
W--> 178 ttgtatagtt gcttatttca agccatacaa aaatntaatt tgcatacttt attgtcatga 180
W--> 180 ttagaaagaa canaaccatg tgtgtttcca agcataaaan aataagacca aaactttcac 240
W--> 182 cagtcgtgct cnttttttct ttgagggtta tatatatata tatatatata tatatatata 300
W--> 184 tatatatata tatatatata tatatatata tanagaatca taacatgttt tgatagggtac 360
186 atgataagaa atggatcatt cagttaataa cattttttaa tatactatac aatgcttaca 420
W--> 188 tcctagagat acatatatta taccatcatg cacnaaacct gagagaaatt tagtactata 480
W--> 190 tcacgagaaa gacacatgcc tttctgtttg tcctattatc attataanan aaacttggna 540
192 ttaaacatac agcacaattc tttgtttatc gtaa 574
195 <210> SEQ ID NO: 9
196 <211> LENGTH: 622
197 <212> TYPE: DNA
198 <213> ORGANISM: Glycine max
200 <223> OTHER INFORMATION: unsure at all n locations
W--> 201 <400> SEQUENCE: 9
W--> 203 tggggatata tgccttgang ttcactnnen atgnetangn ccactatcga gtactcaagc 60
W--> 205 ttgtanatata tactentata cattgcctgt tccattatgc tcttgatgtc ettatatgtt 120
207 acttcgctcg tgacatcttt tgtcttgaat cggaatgaca tgacacggtt atctgtactg 180
W--> 209 tctntnngta ttggtagttg atatcgcggt gcgggaggta attccgattg gattaactca 240
W--> 211 ccataccttaa cttgccanna ttgtatgaca tttgttgttg gatcacctat gatgtcttgt 300
W--> 213 ttccaacggt aatctatatc atttctgatg gcataagcat gaaaccaatc aaagaanagg 360
W--> 215 acattaatct tgactcttct acanantcgt agaactngct tggatttgtg tctgtttgac 420
W--> 217 cctttgtaaa gtggaaaacc atctctttat ggtcattctc cngagaataa aatctttcta 480
W--> 219 anggttnctt atcanntgct aagtgcagat acatcataag gtncataaaa aagtatgttg 540
W--> 221 gattgatega ctttggcgnc tcttgctctg gtgatgtgtc taggatctna aanganctat 600
223 tcttgagtta cagaagactg tg 622
226 <210> SEQ ID NO: 10
227 <211> LENGTH: 250
228 <212> TYPE: DNA
229 <213> ORGANISM: Glycine max
231 <223> OTHER INFORMATION: unsure at all n locations
W--> 232 <400> SEQUENCE: 10
W--> 234 ccttcacccg acgaagacac tgacananac ttatcttctc cttcttggac aaagtatggc 60
W--> 236 aggctgnggg gcaagtaaat ttcttcccat cagaccttgg atgcaactat gatcgtatac 120
W--> 238 ccataatcagc tacatcttga cnggtattca agccatcctt tgtcttgcct ttgaatgtaa 180
W--> 240 ggaacgtccc aatgacacta tcacagacat tnttctccac atgcataaca tcaatacaat 240
242 gtctaacgtc 250
245 <210> SEQ ID NO: 11
246 <211> LENGTH: 536
247 <212> TYPE: DNA
248 <213> ORGANISM: Glycine max
250 <223> OTHER INFORMATION: unsure at all n locations

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W--> 251 <400> SEQUENCE: 11
W--> 253 tgatgncntt nnaattgac gcacgtanta ggtacactat aatactcagc gttcgagaaa   60
W--> 255 ccacttaaac taaggaagtt cctanacaaa aatcaatgga ggaagcttcg ccaagtatgc   120
W--> 257 gcattgaaga cacccttattc aaacctttca agttagtgga gaaggctgaa cgaanacta   180
      259 gggaacttag aacaactaaa tccttaatgg aatgcgtagg tgacaatcat agtgaattac   240
      261 taaacaagat tggtagttac taatggcatt cagatactcc caagcctcga taatacttct   300
W--> 263 aaatgggata agaagacctn cacataataa tgtattaatg aagatgtgac cngactagat   360
      265 aaccactgag atgaatagtg cagaaagata taatccataa ttcaacctga aacacctcaa   420
      267 tattatcacg tcgctgcgctg actctttaga gaagagtaaa caattagagt tagtgaacac   480
W--> 269 tcatgatgac taatgcaacg attactctga tcctcactat actgtgccat acaacn     536
      272 <210> SEQ ID NO: 12
      273 <211> LENGTH: 210
      274 <212> TYPE: DNA
      275 <213> ORGANISM: Glycine max
      277 <400> SEQUENCE: 12
      279 tcatcttgct tggacgatga gaaaactggt gcaaatgaag aggggtgagaa ggatggagaa   60
      281 acccatgctg tgactgtcat tcctatacgg ccaagttccc caccagctca acaccatcat   120
      283 tactcagcca atatcagtc tctctattac ccaccaccca tttatccata aaggctatcc   180
      285 cttaatcaac aacaaaaccc acctaccaca                               210
      288 <210> SEQ ID NO: 13
      289 <211> LENGTH: 397
      290 <212> TYPE: DNA
      291 <213> ORGANISM: Glycine max
      293 <223> OTHER INFORMATION: unsure at all n locations
W--> 294 <400> SEQUENCE: 13
W--> 296 ttgatcatcc tgctntgata aataagaaag cctgggaaaa tggagacaat aagaaggagg   60
      298 gaggaacca tgcgtgtgatt gccgttccta cttggccaaa tttcccacca gctcaacaat   120
      300 gtcaatactc aaccaatate agcccttctc attaccaccc accctattag tcaagaacac   180
W--> 302 ccaatcatcc acaaaggcca cccctgaatc agccacana gcttgcctgcc gcacatncga   240
W--> 304 tactaaacac caccactaac acanaticana acaccaacca gggaanggaa tttcagaaaa   300
      306 taagcctgca gaatcaccca attctggtgc atatgctaac tacttcoatat tactcataat   360
W--> 308 caatggcaca taccaccca nggtctcaac tcattttt                               397
      311 <210> SEQ ID NO: 14
      312 <211> LENGTH: 548
      313 <212> TYPE: DNA
      314 <213> ORGANISM: Glycine max
      316 <223> OTHER INFORMATION: unsure at all n locations
W--> 317 <400> SEQUENCE: 14
W--> 319 ngatgtgagg aagtgtggaa gagtcagtct tcctactntt gtttgttgac catatatattg   60
W--> 321 tacctggaga tatgtcgcan gggtcacgag acctctgtga ggtcagggtg agtgctatnt   120
W--> 323 cccaaaacca agcttgacca atcccaaccc aacctgngca tattcagtcg gtgtgaacct   180
W--> 325 gtgacgtacc taagcaggcg agcttctgac agtcaaccca tattagaaca aagaccacan   240
      327 agcaaggagg ctgctgtggc agctggccag ctatggatct tgagtgggtat ctggagatag   300
      329 gcctctcgta atcgattacc caggggtgtg aatcgattac atgggctaca aatggagacc   360
      331 agaagttaag atggcctctg ggtatcgatt accaacgggt gtgtaatcga ttaccatgct   420
W--> 333 tannaatgga nacagnagat taagatggcc tctggtatcc attaccaacg ggtgtaacga   480
W--> 335 tacanagcta aacatgagac ggatgtgcgn ggctctgtat ccataaccat gatattattca   540
W--> 337 ataccaan                               548
      340 <210> SEQ ID NO: 15

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341 <211> LENGTH: 598
342 <212> TYPE: DNA
343 <213> ORGANISM: Glycine max
345 <223> OTHER INFORMATION: unsure at all n locations
W--> 346 <400> SEQUENCE: 15
348 tatatgtact tgacnecgtc atctctgagt cacctgcggc atgcaagctt anaaatatat 60
W--> 350 ggngattatg tnttggtatg tatgaattac atcacagata atttgattga ctaagattaa 120
352 gtgatgatgg tgggtgtaga tctgatgacc atcacagtga agaccacagt gatggtgggt 180
354 gcaagcatgg agctgaagag gaacatgaaa ctaatatatg tgatttgaca gggagcacac 240
356 aaaggttctg cattgcggca gtgaagaaca tgcttttgat ttctatacta gatatgccag 300
358 atgtcatggg ttggatgtga gaaaatatga catacttcga gaatttgaat ggggaatgta 360
W--> 360 taaaacattg gttttcttgc atagaanagg gttgagaaaa aagaacactt cagcagggtc 420
362 gatagaataa gagacatata tattcatact aattgtgagc taggctcatg ttctcttagat 480
364 agaaacataa catgaaagtc tttattcaca gaatataaca tgactacca cactgtatt 540
W--> 366 atatatccaa gatcgggata ctatttgata actagcngat agtgataatt gtgtgacn 598
369 <210> SEQ ID NO: 16
370 <211> LENGTH: 226
371 <212> TYPE: DNA
372 <213> ORGANISM: Glycine max
374 <223> OTHER INFORMATION: unsure at all n locations
W--> 375 <400> SEQUENCE: 16
377 gtgtacacat gttgtaactt tcttgaatga aagtcttatg agatacaatt canagtcca 60
W--> 379 cttctctccc tctnttatcc cttcaatncc gtgctcccgc cttctctctn tcttttcttc 120
381 cattaaagta tctctctcaa gcttcttacc caaggccaat tgtgtgtggtg aagctccttc 180
383 ttccttggct gattccctag tggatgggtc caccctcttc ctcttc 226
386 <210> SEQ ID NO: 17
387 <211> LENGTH: 193
388 <212> TYPE: DNA
389 <213> ORGANISM: Glycine max
391 <223> OTHER INFORMATION: unsure at all n locations
W--> 392 <400> SEQUENCE: 17
394 atgacattnt aattctgcaa ataacaataa ctaaacctt tatgtactag attagagact 60
W--> 396 aaagaaaggg attntttctt tctttttctt cattcgtggc tttatccctt gacatttact 120
W--> 398 agacttgtgc ttccacatca tatatcccta tcattctgtc tttaatcatt canaaattca 180
400 ttgatcttg tct 193
403 <210> SEQ ID NO: 18
404 <211> LENGTH: 157
405 <212> TYPE: DNA
406 <213> ORGANISM: Glycine max
408 <223> OTHER INFORMATION: unsure at all n locations
W--> 409 <400> SEQUENCE: 18
411 ttaagttaaa aagtcttttt tcaacaaatt actctctggt aatcgattac cagaggatgt 60
W--> 413 aatcgattac cagtggccaa aactgantta caacagctat taaaatntga attcaaaatt 120
415 tgcactgtgt aatcgattac acatatatgg taatcga 157
418 <210> SEQ ID NO: 19
419 <211> LENGTH: 406
420 <212> TYPE: DNA
421 <213> ORGANISM: Glycine max
423 <400> SEQUENCE: 19

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:18 M:283 W: Missing Blank Line separator, <400> field identifier
L:20 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:20 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:20 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:20 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:22 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:22 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:22 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:24 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:24 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:24 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:28 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:28 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:28 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:30 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:30 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:30 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:34 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:34 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:34 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:36 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:36 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:36 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:49 M:283 W: Missing Blank Line separator, <400> field identifier
L:63 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:63 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:63 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:63 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:65 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:65 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:65 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:88 M:283 W: Missing Blank Line separator, <400> field identifier
L:90 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:90 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:90 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:90 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:94 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:94 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:94 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:96 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4

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L:96 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:96 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:107 M:283 W: Missing Blank Line separator, <400> field identifier
L:111 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:111 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:111 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:111 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:117 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:117 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:117 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:119 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:119 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:119 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:128 M:283 W: Missing Blank Line separator, <400> field identifier
L:130 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:130 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:130 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:145 M:283 W: Missing Blank Line separator, <400> field identifier
L:147 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
M:340 Repeated in SeqNo=7
L:172 M:283 W: Missing Blank Line separator, <400> field identifier
L:174 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
M:340 Repeated in SeqNo=8
L:201 M:283 W: Missing Blank Line separator, <400> field identifier
L:203 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
M:340 Repeated in SeqNo=9
L:232 M:283 W: Missing Blank Line separator, <400> field identifier
L:234 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:251 M:283 W: Missing Blank Line separator, <400> field identifier
L:253 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
M:340 Repeated in SeqNo=11
L:294 M:283 W: Missing Blank Line separator, <400> field identifier
L:296 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:317 M:283 W: Missing Blank Line separator, <400> field identifier
L:319 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
M:340 Repeated in SeqNo=14
L:346 M:283 W: Missing Blank Line separator, <400> field identifier
L:348 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:375 M:283 W: Missing Blank Line separator, <400> field identifier
L:377 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
M:340 Repeated in SeqNo=16
L:392 M:283 W: Missing Blank Line separator, <400> field identifier
L:394 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
M:340 Repeated in SeqNo=17
L:409 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY

DATE: 06/07/2000

PATENT APPLICATION: US/09/521,640

TIME: 11:22:32

Input Set : D:\BACENDTAB_FINAL_RETREATS.rpt

Output Set: N:\CRF3\06072000\I521640.raw

L:413 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:478 M:283 W: Missing Blank Line separator, <400> field identifier
L:480 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
M:340 Repeated in SeqNo=22
L:501 M:283 W: Missing Blank Line separator, <400> field identifier
L:503 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23
M:340 Repeated in SeqNo=23
L:522 M:283 W: Missing Blank Line separator, <400> field identifier
L:526 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24
L:535 M:283 W: Missing Blank Line separator, <400> field identifier
L:537 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
M:340 Repeated in SeqNo=25
L:576 M:283 W: Missing Blank Line separator, <400> field identifier
L:580 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27
M:340 Repeated in SeqNo=27
L:595 M:283 W: Missing Blank Line separator, <400> field identifier
L:597 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
M:340 Repeated in SeqNo=28
L:618 M:283 W: Missing Blank Line separator, <400> field identifier
L:620 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29
M:340 Repeated in SeqNo=29
L:649 M:283 W: Missing Blank Line separator, <400> field identifier
L:651 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:30
M:340 Repeated in SeqNo=30
L:668 M:283 W: Missing Blank Line separator, <400> field identifier
L:670 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31
M:340 Repeated in SeqNo=31
L:687 M:283 W: Missing Blank Line separator, <400> field identifier
L:693 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
L:724 M:283 W: Missing Blank Line separator, <400> field identifier
L:726 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
M:340 Repeated in SeqNo=34
L:741 M:283 W: Missing Blank Line separator, <400> field identifier
L:758 M:283 W: Missing Blank Line separator, <400> field identifier
L:787 M:283 W: Missing Blank Line separator, <400> field identifier
L:810 M:283 W: Missing Blank Line separator, <400> field identifier
L:839 M:283 W: Missing Blank Line separator, <400> field identifier
L:860 M:283 W: Missing Blank Line separator, <400> field identifier
L:891 M:283 W: Missing Blank Line separator, <400> field identifier
L:908 M:283 W: Missing Blank Line separator, <400> field identifier
L:945 M:283 W: Missing Blank Line separator, <400> field identifier
L:964 M:283 W: Missing Blank Line separator, <400> field identifier
L:981 M:283 W: Missing Blank Line separator, <400> field identifier
L:1010 M:283 W: Missing Blank Line separator, <400> field identifier
L:1031 M:283 W: Missing Blank Line separator, <400> field identifier
L:1060 M:283 W: Missing Blank Line separator, <400> field identifier
L:1093 M:283 W: Missing Blank Line separator, <400> field identifier
L:1114 M:283 W: Missing Blank Line separator, <400> field identifier
L:1149 M:283 W: Missing Blank Line separator, <400> field identifier

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Output Set: N:\CRF3\06072000\I521640.raw

L:1168 M:283 W: Missing Blank Line separator, <400> field identifier
L:1197 M:283 W: Missing Blank Line separator, <400> field identifier
L:1260 M:283 W: Missing Blank Line separator, <400> field identifier
L:1301 M:283 W: Missing Blank Line separator, <400> field identifier
L:1330 M:283 W: Missing Blank Line separator, <400> field identifier
L:1359 M:283 W: Missing Blank Line separator, <400> field identifier